



**University of  
Zurich**<sup>UZH</sup>

**Zurich Open Repository and  
Archive**

University of Zurich  
University Library  
Strickhofstrasse 39  
CH-8057 Zurich  
[www.zora.uzh.ch](http://www.zora.uzh.ch)

---

Year: 2017

---

## **Complete genome of *Enterobacter cloacae* 704SK10, an OXA-48 encoding wastewater isolate**

Marti, Roger ; Stephan, Roger ; Klumpp, Jochen ; Nüesch-Inderbinen, Magdalena ; Hummerjohann, Jörg ; Bagutti, Claudia ; Zurfluh, Katrin

**Abstract:** Here we present the complete genome sequence of *Enterobacter cloacae* 704SK10, a Swiss wastewater isolate encoding an OXA-48 carbapenemase. Assembly resulted in closed sequences of the 4,876,946-bp chromosome, a 111,184-bp IncF plasmid, and an OXA-48-encoding IncL plasmid (63,458 bp) nearly identical to the previously described plasmid pOXA-48.

DOI: <https://doi.org/10.1128/genomeA.00830-17>

Posted at the Zurich Open Repository and Archive, University of Zurich

ZORA URL: <https://doi.org/10.5167/uzh-148759>

Journal Article

Published Version

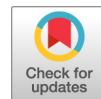


The following work is licensed under a Creative Commons: Attribution 4.0 International (CC BY 4.0) License.

Originally published at:

Marti, Roger; Stephan, Roger; Klumpp, Jochen; Nüesch-Inderbinen, Magdalena; Hummerjohann, Jörg; Bagutti, Claudia; Zurfluh, Katrin (2017). Complete genome of *Enterobacter cloacae* 704SK10, an OXA-48 encoding wastewater isolate. *Genome Announcements*, 5(33):e00830-17.

DOI: <https://doi.org/10.1128/genomeA.00830-17>



# Complete Genome Sequence of *Enterobacter cloacae* 704SK10, an OXA-48-Encoding Wastewater Isolate

Roger Marti,<sup>a</sup> Roger Stephan,<sup>a</sup>  Jochen Klumpp,<sup>b</sup> Magdalena Nüesch-Inderbinnen,<sup>a</sup> Jörg Hummerjohann,<sup>c</sup> Claudia Bagutti,<sup>d</sup> Katrin Zurfluh<sup>a</sup>

Institute for Food Safety and Hygiene, Vetsuisse Faculty University of Zurich, Zurich, Switzerland<sup>a</sup>; Institute of Food, Nutrition and Health, ETH Zurich, Zurich, Switzerland<sup>b</sup>; Division of Food Microbial Systems, Microbiological Safety of Foods of Animal Origin Group, Agroscope, Bern, Switzerland<sup>c</sup>; Biosafety Laboratory, State Laboratory Basel-City, Basel, Switzerland<sup>d</sup>

**ABSTRACT** Here we present the complete genome sequence of *Enterobacter cloacae* 704SK10, a Swiss wastewater isolate encoding an OXA-48 carbapenemase. Assembly resulted in closed sequences of the 4,876,946-bp chromosome, a 111,184-bp IncF plasmid, and an OXA-48-encoding IncL plasmid (63,458 bp) nearly identical to the previously described plasmid pOXA-48.

*Enterobacter cloacae* is ubiquitous in the environment and can be a part of the commensal flora of human and animal gastrointestinal tracts (1). It is also an important opportunistic pathogen associated with nosocomial infections (2) and the third most common species of enterobacteria carrying the class D  $\beta$ -lactamase OXA-48, after *Klebsiella pneumoniae* and *Escherichia coli* (3). OXA-48 is not susceptible to  $\beta$ -lactamase inhibitors, and it hydrolyzes penicillins at high rates and carbapenems at significant, yet low, rates. Although extended-spectrum cephalosporins are not hydrolyzed by this enzyme (4), OXA-48 producers (exclusively enterobacteria [4]) often express extended-spectrum  $\beta$ -lactamases (ESBL) in addition to OXA-48, rendering all  $\beta$ -lactam antibiotics ineffective against such strains (5).

*E. cloacae* 704SK10 was isolated from wastewater near Basel, Switzerland, in December 2015 (6). As the strain tested positive for OXA-48 and was phenotypically resistant to cefotaxime (CTX), it was fully sequenced. We used Pacific Biosciences (PacBio) single-molecule real-time (SMRT) technology RS2 reads with C4/P6 chemistry to sequence the strain (Functional Genomics Center Zurich) and *de novo* assembled the genome using SMRTAnalysis 2.3 (HGAP3 protocol). The MLST-1.8 server (7), ResFinder 2.1 (8), and PlasmidFinder 1.3 (9) (see <http://www.genomicepidemiology.org/>) were used for initial assessment of sequence type (ST), acquired antibiotic resistances, and plasmid incompatibility (Inc) groups.

The assembly resulted in one chromosome and two plasmids (all sequences are closed), which were automatically annotated using the NCBI Prokaryotic Genome Annotation Pipeline (10). The chromosome is 4,876,946 bp long with a GC content of 55.9% and encodes genes for  $\beta$ -lactam (*bla*<sub>MIR-15</sub>) and fosfomycin (*fosA*) resistance. The strain belongs to ST272, which is not among the high-risk clones identified in a recent study (11). The larger plasmid, p704SK10\_1 (IncF), is 111,184 bp in size with a G+C content of 50.9% and encodes no acquired antibiotic resistance genes. The 63,458-bp OXA-48-encoding IncL plasmid p704SK10\_2 (G+C content, 51.2%) is nearly identical to pOXA-48 (GenBank accession no. JN626286), the prototype of highly similar IncL plasmids responsible for the dissemination of OXA-48 (5, 12). The two plasmids are 99.7% identical at the nucleotide (nt) level apart from two insertions in p704SK10\_2,

Received 3 July 2017 Accepted 7 July 2017 Published 17 August 2017

**Citation** Marti R, Stephan R, Klumpp J, Nüesch-Inderbinnen M, Hummerjohann J, Bagutti C, Zurfluh K. 2017. Complete genome sequence of *Enterobacter cloacae* 704SK10, an OXA-48-encoding wastewater isolate. Genome Announc 5:e00830-17. <https://doi.org/10.1128/genomeA.00830-17>.

**Copyright** © 2017 Marti et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Katrin Zurfluh, [katrin.zurfluh@uzh.ch](mailto:katrin.zurfluh@uzh.ch).

which both encode insertion element IS1 protein InsB (WP\_001119291.1). The first insertion (777 bp) is 163 bp upstream of the gene encoding OXA-48, and the second one (776 bp) is 356 bp downstream of *korC*, disrupting a hypothetical protein.

*E. cloacae* 704SK10 is another isolate that demonstrates the importance and high degree of conservation of pOXA-48-like IncL plasmids in the dissemination of this carbapenemase in enterobacteria.

**Accession number(s).** Sequence and annotation data of the *E. cloacae* 704SK10 genome have been deposited at GenBank under accession numbers [CP022148](#) (chromosome), [CP022149](#) (p704SK10\_1), and [CP022150](#) (p704SK10\_2). This is the first version of this genome.

## ACKNOWLEDGMENT

This work was supported by funding from the University of Zurich.

## REFERENCES

1. Davin-Regli A, Pagès JM. 2015. *Enterobacter aerogenes* and *Enterobacter cloacae*; versatile bacterial pathogens confronting antibiotic treatment. *Front Microbiol* 6:392. <https://doi.org/10.3389/fmicb.2015.00392>.
2. Mezzatesta ML, Gona F, Stefani S. 2012. *Enterobacter cloacae* complex: clinical impact and emerging antibiotic resistance. *Future Microbiol* 7:887–902. <https://doi.org/10.2217/fmb.12.61>.
3. Potron A, Poirel L, Rondinaud E, Nordmann P. 2013. Intercontinental spread of OXA-48 beta-lactamase-producing *Enterobacteriaceae* over a 11-year period, 2001 to 2011. *Euro Surveill* 18:31. pii: 20549. <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=20549>.
4. Poirel L, Potron A, Nordmann P. 2012. OXA-48-like carbapenemases: the phantom menace. *J Antimicrob Chemother* 67:1597–1606. <https://doi.org/10.1093/jac/dks121>.
5. Poirel L, Bonnin RA, Nordmann P. 2012. Genetic features of the wide-spread plasmid coding for the carbapenemase OXA-48. *Antimicrob Agents Chemother* 56:559–562. <https://doi.org/10.1128/AAC.05289-11>.
6. Zurfluh K, Bagutti C, Brodmann P, Alt M, Schulze J, Fanning S, Stephan R, Nüesch-Inderbinen M. 2017. Wastewater is a reservoir for clinically relevant carbapenemase and 16S rRNA methylase producing *Enterobacteriaceae*. *Int J Antimicrob Agents*. <https://doi.org/10.1016/j.ijantimicag.2017.04.017>.
7. Larsen MV, Cosentino S, Rasmussen S, Friis C, Hasman H, Marvig RL, Jelsbak L, Sicheritz-Pontén T, Ussery DW, Aarestrup FM, Lund O. 2012. Multilocus sequence typing of total-genome-sequenced bacteria. *J Clin Microbiol* 50:1355–1361. <https://doi.org/10.1128/JCM.06094-11>.
8. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 67:2640–2644. <https://doi.org/10.1093/jac/dks261>.
9. Carattoli A, Zankari E, García-Fernández A, Voldby Larsen M, Lund O, Villa L, Møller Aarestrup F, Hasman H. 2014. *In silico* detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. *Antimicrob Agents Chemother* 58:3895–3903. <https://doi.org/10.1128/AAC.02412-14>.
10. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res* 44: 6614–6624. <https://doi.org/10.1093/nar/gkw569>.
11. Izdebski R, Baraniak A, Herda M, Fiett J, Bonten MJ, Carmeli Y, Goossens H, Hryniewicz W, Brun-Buisson C, Gniadkowski M; MOSAR WP2, WP3, and WP5 Study Groups. 2015. MLST reveals potentially high-risk international clones of *Enterobacter cloacae*. *J Antimicrob Chemother* 70:48–56. <https://doi.org/10.1093/jac/dku359>.
12. Carattoli A, Seiffert SN, Schwendener S, Perreten V, Endimiani A. 2015. Differentiation of IncL and IncM plasmids associated with the spread of clinically relevant antimicrobial resistance. *PLoS One* 10:e0123063. <https://doi.org/10.1371/journal.pone.0123063>.